

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 2645.71 Seconds

(Without alignments)
1579.326 Million cell updates/sec

Title: US-09-698-781-3
Perfect score: 1436

Sequence: 1 MKOILHPALLETMTLFPVL.....KHOLVRSKASCNSNSIY 258

Scoring table: BIOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV-xlh
-O=/cgn2_1/USPFO.spool/US09698781/runat_07032003.083459.5329/app.query.fasta.1.654
-DB-EST -QFMT-fastlap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-Biosum62 -TRANS-human40.cdi -LIST-45
-DOCALLIGN-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pio -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER=US09698781 @CGN.1.1.2463 @runat_07032003.083459.5329 -NCPU-6 -ICPU-3
-NO_XLPRY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV.TIMEOUT-120
-MARK.TIMEOUT-30 -THRAD-1 -XGAPOP-10 -XGAPEXT-0.5 -Fgapop-6 -Fgapext-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estio:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_yrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	965	67.2	547	9 AL703262	AL703262 DKF2P686K
2	943	65.7	1037	13 BM554122	BM554122 DKF2P686K
3	943	65.7	1108	13 BM552843	BM552843 AGENCOURT
4	912	63.5	1063	13 BM559790	BM559790 AGENCOURT
5	869	60.5	803	13 BM826346	BM826346 AGENCOURT
6	867	60.4	450	12 BF897404	BF897404 IL2-MT018
7	867	60.4	808	13 BM826697	BM826697 603077463
8	858	59.7	462	12 BF897377	BF897377 IL2-MT018
9	858	59.7	781	13 BM829771	BM829771 603079842
10	850	59.2	464	12 BF897410	BF897410 IL2-MT018
11	830	57.8	451	12 BF897412	BF897412 IL2-MT018
12	825	57.5	443	12 BF897401	BF897401 IL2-MT018
13	823.5	57.3	904	13 BM830749	BM830749 603075145
14	814	56.7	420	12 BF897378	BF897378 IL2-MT018
15	814	56.7	784	13 BM825564	BM825564 603072524
16	807.5	56.2	946	13 BM832357	BM832357 603072889
17	796	55.4	454	12 BF897368	BF897368 IL2-MT018
18	782.5	54.5	728	13 BM827352	BM827352 603077880
19	780	54.3	806	13 BM826010	BM826010 603076409
20	772.5	53.8	1414	11 AK009449	AK009449 Mus muscu
21	769	53.6	406	12 BF897379	BF897379 IL2-MT018
22	762	53.1	952	12 BG721420	BG721420 602694975
23	761.5	53.0	784	13 BM829333	BM829333 603079465
24	761.5	53.0	864	13 BM460544	BM460544 603201164
25	758	52.8	801	12 BG722432	BG722432 602693657
26	748	52.1	760	13 BM831850	BM831850 603078978
27	741	51.6	764	13 BM829788	BM829788 603079859
28	740	51.5	742	12 BG723701	BG723701 602697894
29	739	51.5	722	13 BM460734	BM460734 603204913
30	737	51.3	730	13 BM559392	BM559392 603253072
31	736	51.3	721	13 BM830127	BM830127 603072754
32	729	50.8	769	13 BM825992	BM825992 603075580
33	719.5	50.1	865	12 BG721972	BG721972 602696722
34	710.5	49.5	708	13 BM156058	BM156058 603254682
35	707	49.2	740	12 BG724382	BG724382 602692860
36	706.5	49.2	821	12 BG722866	BG722866 602695346
37	706	49.2	401	12 BF897366	BF897366 IL2-MT018
38	696	48.5	852	13 BM553721	BM553721 603190658
39	695.5	48.4	843	12 BG723588	BG723588 602694310
40	692.5	48.2	705	13 BM683698	BM683698 603306249
41	689.5	48.0	769	13 BM464694	BM464694 603202325
42	679.5	47.3	849	13 BM562149	BM562149 603255338
43	673.5	46.9	600	10 BE588308	BE588308 196937 BA
44	671.5	46.8	674	13 BM691604	BM691604 603307276
45	670	46.7	870	13 BM465248	BM465248 603204748

ALIGNMENTS

RESULT 1
LOCUS AL703262 547 bp mRNA linear EST 22-MAR-2002
DEFINITION DKF2P686K1819-r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
ACCESSION AL703262
VERSION AL703262.1 GI:19686617
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann
TITLE EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann

JOURNAL
COMMENT

,S.)
(1999)
Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestrase 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Cloned from S. Miesmann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZ686K1819) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES

source
1..547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ686K1819"
/clone_1lb="686 (synonym: hicc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: Sflra; Site_2: Sflib;
cDNA-collection"

BASE COUNT 170 a 120 c 120 g 137 t
ORIGIN

Alignment Scores:

Pred. No.: 5.98e-99 Length: 547
Score: 965.00 Matches: 179
Percent Similarity: 98.90% Conservative: 0
Best Local Similarity: 98.90% Mismatches: 2
Query Match: 67.20% Indels: 0
DB: 9 Gaps: 0

US-09-698-781-3 (1-258) x AL703262 (1-547)

QY 1 MetTSGInIleuHISProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20
|||||
DB 4 ATGAACAACAAATCTCTCTCTGGAACACACGCAATGACATTTATCCAGTCTG 63
QY 21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
|||||
DB 64 TTGTTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 123
QY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
|||||
DB 124 TTTACTGCTTTTAAACCCCAACACAGTGCAGAAAGGAGATTTGTAATAAGCACAT 183
QY 61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluThrPheAsn 80
|||||
DB 184 GAACGAGAGAGAGAGATCTCCCTGCCAGAAACATCTGAAAGATGGAATGGAACAAA 243
QY 81 GluAlaAlaAlaAsnAlaGlnLysThrPheAlaAsnGlnCysAsnThrArgHisSerAsnPro 100
|||||
DB 244 GAGGCTGCAGCAAAATGCCCAAGAGTGGCAACCACTGCAATTAACGACAGTAACCA 303
QY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuLysMetSerSerAlaProSer 120
|||||
DB 304 AAGGATCGAATGACAAAGTAAATGTGCTGAGAAATCTTACATGTCGAAGTGCCTCAGC 363
QY 121 SerTPSPSerGlnAlaIleGlnSerTPPheAspGluThrAsnAspPheAspPheGlyVal 140
|||||
DB 364 TCATGGTGCAGCAATCCAAAGCTGGTTGATGATACAAATGATTTTACCTTGGTGA 423
QY 141 GlyProLysThrProAsnAlaValAlaGlyHisTyrThrGlnValValTrrPyrSerSer 160
|||||

DB 424 GGGCCAAACGTCGCCAGCTGTTGGACATTTATACACAGCTTTGTTGACTCTTCA 483
QY 161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGluLysValLeuLysTyrTyr 180
|||||
DB 484 TACCTCGGTGATGTGGAAATGCTACTCTCCCAATCAAAAAGTTCTAAATACACTAT 543

QY 181 Val 181
|||
DB 544 GTT 546

RESULT 2
BMS54122 1037 bp mRNA linear EST 20-FEB-2002
LOCUS BMS54122
DEFINITION AGENCOURT_6546919 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742354
5', mRNA sequence.
ACCESSION BMS54122
VERSION BMS54122.1 GI:18793449
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1037)
NIH-MGC http://mhc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bhs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12760 row: f column: 19
High quality sequence stop: 385.
Location/Qualifiers

FEATURES

source

1..1037
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5742354"
/clone_1lb="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH-MGC Library."

BASE COUNT 318 a 223 c 228 g 266 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 5.27e-96 Length: 1037
Score: 943.00 Matches: 177
Percent Similarity: 78.63% Conservative: 29
Best Local Similarity: 67.56% Mismatches: 50
Query Match: 65.67% Indels: 6
DB: 13 Gaps: 3

US-09-698-781-3 (1-258) x BMS54122 (1-1037)

QY 1 MetTSGInIleuHISProAlaLeuGluThrThr-----AlaMetThrLeuPhePr 18
|||||
DB 153 ATAAAGTAAATTTTCTCTCTCTGCAAAACACATTTCCAGCAATGCTTTACTACC 212
QY 18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
|||||

Db 213 GGGG---TTGTTCTGTTACTGTGCTGCTTCCATCTTACTGCA---GAAGGAAGA 266
 Oy 38 pProAlaPheThrAlaLeuLeuThrThGlnThrGlnValGlnArgGluIleValAla 58
 Db 267 TCCCCCTTTACTGCTTTGTTTAACCAACCCAGTTCAGCAAGGAGAAAGGAGATGTAATTA 326
 Oy 58 sHisAsnGluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLeuMetGluTr 78
 Db 327 ACACAGTAAGTAAGCAAGAGTCTCTCCACCTGCCAATAACATGCTAAAGTAAGTAAG 386
 Oy 78 pAsnIleGluAlaAlaAlaAsnAlaGlnIleStrpAlaAsnGlnCysAsnTyrArgHisSe 98
 Db 387 GAGCAGAGAGGTAACAGCAATGCCCCAAGGGGCAACCAAGTGCACCTTACACATAG 446
 Oy 98 rAsnProLysAspArgMetThrSerLeuLysCysGluGlnAsnLeuTyrMetSerSerAl 118
 Db 447 TGATCCAGAGGAGCCCAAAACAGTACAGATGTGTGAGAACTCTATATGTCAAGTGA 506
 Oy 118 aProSerSerTPSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAsp 138
 Db 507 CCTACTCTCTGCTGCTCTGCAATCCAAAGCTGTGATGAGAGATCCCTAGATTGTCTTA 566
 Oy 138 eGlyValGlyProLysThrProAsnAlaValAlaGlyHisTyrThrGlnValValTyrPty 158
 Db 567 TGGTGTAGACCAAGAGAGCCCAATGCACTGTGTGACATTTACTACACTGTGTGGTA 626
 Oy 158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyr 178
 Db 627 CTCGACTTCCAGCAGCGAGGTGTGGAATTCCTACTGTCCTCCCAATCAAGATAGCTCA 686
 Oy 178 rTyrTyrValCysGlnIleTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProty 198
 Db 687 CTACTATGTTTCCCATATGTTCTGCTGCTGNTATATGAAATGAAAGAAATACCCGTA 746
 Oy 198 rGluGlnGly-AlaProCysAlaSerCysProAspAsnCysAspArgLysLeuCysThra 218
 Db 747 CCACACAGGAACACCTGTGCGGTTGCCGTGATGACGTGGACAAAGCATATGACACA 806
 Oy 218 srGlyCysLysTyrGluAspLeuTyrSerAsnLysSerLeuLysLeuThrThc 238
 Db 807 AATAGTCCAGATCAAGATCTCCTAAGTACTGATTCCTGAAGAAATACAGCTGGCT 866
 Oy 238 yLysHisGlnLeuValAlaArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleT 258
 Db 867 GTGACATAGATTACTCAAGGAAGGCAAGGCTACTTGCCTATGTGACAGCAAAATTT 926
 Oy 258 yr 258
 Db 927 AC 928
 RESULT 3
 LOCUS BM552843 1108 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6542520 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742685
 5' mRNA sequence.
 ACCESSION BM552843
 VERSION BM552843.1 GI:18791053
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1108)
 AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM12761 row: d column: 14
 High quality sequence stop: 700.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5742685"
 /clone_11b="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."
 BASE COUNT 341 a 236 c 235 g 291 t 5 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5 87e-96 Length: 1108
 Score: 943.00 Matches: 172
 Percent Similarity: 82.57% Conservative: 27
 Best Local Similarity: 71.37% Mismatches: 40
 Query Match: 65.67% Indels: 3
 DB: 13 Gaps: 2
 US-09-698-781-3 (1-258) x BM552843 (1-1108)
 Oy 13 AlaMetThrLeuPheProValLeuLeuPheLeuValAlaGlyLeuLeuProSerPhePro 32
 Db 136 GCAATGGCTTACTACTACCGG---TTGTTCTGTTACTGTGCTGCTCCATCTTACT 192
 Oy 33 AlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGlnValGln 52
 Db 193 GCA---GAAGGAAGATCCCGCTTACTGCTTTTAAACCAAGTGTGCAAGTGA 249
 Oy 53 ArgGluIleValAsnLysHisAsnGluLeuArgArgAlaValSerProProAlaAsn 72
 Db 250 AGGAGATTTGTAATAACACATGAACATAGAAAGCACTCTCCACTGCAATAC 309
 Oy 73 MetLeuLysMetGluTrpAsnLysGluAlaAlaAsnAlaGlnIleStrpAlaAsnGln 92
 Db 310 ATGCTAAGATGGATGAGAGCAGAGAGTAAACCAAGATGCCCAAGGTGGCAACAG 369
 Oy 93 CysAsnTyrArgHisSerAsnProLysAspArgMetThrSerLeuLysCysGluGln 112
 Db 370 TGACCTTACACATAGTGTGTCAGAGAGCCGCAAAACGTCACAGATGTGTGCAAT 429
 Oy 113 LeuTyrMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGlu 132
 Db 430 CTCTATATGCAAGTACCTACTCTCTGCTCTTGCACATCCAAAGCTGTGATGACGAG 489
 Oy 133 TyrAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaValAlaGlyHisTyr 152
 Db 490 ATCTAGATTGTTCTATGTTGTGAGACCAAGAGTCCCAATGCTGTGACATTTA 549
 Oy 153 ThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGlnAsnAlaTyrCysProAsn 172
 Db 550 ACTCAGCTTGTGTGACTGCTTACCCAGAGTGGCTGTGCAATTTGCTTCTCCCAAT 609
 Oy 173 GlnLysValLeuLysTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsn 192
 Db 610 CAGATAGCTTAATAACTACTATGTTGCCAATATGCTCTGCTGTAATATGAAT 669
 Oy 193 ArgLeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysProAspAsnCys 212
 Db 670 AGAAGATACCCCTACCAACAAAGAACACTTGTGCGGTGCTGCTGCTGATGCTGAC 729

Oy	213	AspG11leucCysThrAnsglyCysLysTyRgluAspLeuTySerAnsgLysSerLeu	232
Db	730	MAAGGACTATGCACCAATGTTCCAGATGCTTAAGTAACGTGATTCCTTG	789
Oy	233	LysLeuThrLeuThrcysLysHisGlnLeuValArgAspSerCysLysAlaSerCysAsn	252
Db	790	AGATACACACTGCG-TGTGAACATGAGTACTTACCAAGAAAGTGCAGGCTACTTCC	848
Oy	253	Cys 253	
Db	849	TGT 851	
RESULT 4			
LOCUS	BM559790	1063 bp	mRNA linear EST 20-FEB-2002
DEFINITION	AGENCOURT_6565524 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744414		
ACCESSION	BM559790		
VERSION	BM559790.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1063)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: L1AM12765 row: 1 column: 15 High quality sequence stop: 618. Location/Qualifiers 1. 1063 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5744414" /clone_lib="NIH_MGC_119" /tissue_type="medulla" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-SPORT6; Site:1; Note: Site:2: EcoRV (destroyed): RNA source normal medulla from anonymous male age 27. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library." BASE COUNT 317 a 235 c 240 g 271 t ORIGIN		
Alignment Scores:			
Pred. No.:	1,79e-92	Length:	1063
Score:	912.00	Matches:	170
Percent Similarity:	80.42%	Conservative:	23
Best Local Similarity:	70.83%	Mismatches:	44
Query Match:	63.51%	Indels:	4
DB:	13	Gaps:	2
Oy	13	AlaMetThrLeuPheProValLeuLeuPheLeuValAlaGlyLeuLeuProSerPhePro	32
Db	172	GCAATGCTTACTACTACCGGTG--TTGTTTCTGTGCTGCTGCTTCCATTTCTACT	228

FEATURES	LOCATION/Qualifiers
33	AlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGln 52
229	GCA---GAAGGAAGAAGATCCCGCTTTTACTGCTTTTGTAAACCAACAGTTGGCAAGTGCA 285
53	ArgGluIleValAsnLysHisAsnGluLeuValArgAlaValSerProProAlaIleAsn 72
286	AGGAGAGATTGTATAATAACCAATGAACTAGAGAAAGACATCTCTCCACTGCCAATAAC 345
73	MetLeuLysMetCyluTrpAsnLysGluAlaAlaAlaAlaAsnIleGlnLysTrpAlaAsnGln 92
346	ATCTTAAGATGGAATGGAGACAGAGAGGTAAACAACCAATGCCCAAGGTGGCAAAACAG 405
93	CysAsnTyrArgHisSerAsnProLysAspArgMetThrSerLeuLysCysGluGluAsn 112
406	TGCACCTTAAACAATATGGTATATCCAGAGGACCCGCAAAACAGTAAACAAGATGTGTGAGAT 465
113	LeuTyrMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGlu 132
466	CTGTATATGTCAAGTGACCCCTACTTCTGTCTGTCTGTCAATCCAAAGCTGGTATGACGAG 525
133	TyrAsnAspPheAspPheGluValGlyProLysThrProAsnAlaValAlaGlnHisTyr 152
526	ATCCGTGATTTGTCTATGTATGCTGTAGACCAAGAGAGTCCCAATGCATGTGTGACATTAT 585
153	ThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn 172
586	ACCTCACTTGTGTGTGACTCGACTCGACTCAACGAGTGTGGATTTGCCCTACTGTCCCAT 645
173	GlnLysValLeuLysTyrTyrTyrValLysGlnTyrCysProAlaGlyAsnTrpAlaAsn 192
646	CAAGATAGCTAAATAACTACTATGTTTCCCATATGTCTCTGTGTATTAATATGAT 705
193	ArgLeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysProAspAsn 212
706	AAAGAAATATACCCCGTACCCCAAGAGAACACCTTGTGGCGGGTGCCTGATGACTGTGAC 765
213	AspGlyLeuLysThrAsnLysLysTyrGluAspLeuTyrSerAsnCysLys-Serie 232
766	AAAGGACTATGCAACCAATAGTTGCCAGTATCAAGATCTCCCTAAGAACATGGGAGTTCCT 825
232	ubLysLeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLysAlaSerCys 251
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LOCUS	603076694F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168015 5',
DEFINITION	mRNA sequence.
ACCESSION	BI826346
VERSION	BI826346.1 GI:15937896
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota, Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LAM1417 row: k column: 24 High quality sequence stop: 799.

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/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT      250 a      183 c      166 g      204 t
ORIGIN

Alignment Scores:
Pred. No.:      8.45e-88      Length:      803
Score:          869.00      Matches:      160
Percent Similarity: 80.62%      Conservative: 23
Best Local Similarity: 70.48%      Mismatches: 41
Query Match:    60.52%      Indels:      3
DB:             13      Gaps:      2

US-09-698-781-3 (1-258) x B1826346 (1-803)
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Db 127 ATAAAGTAGATATTTCATCTCTCCAGAAACCAATTTCCAGCAATGGCTTTACTACC 186
Oy 20 LeuLeuPheLeuValaIaGlyLeuLeuProSerPheProAlaAsnGlnuAspLysAspPro 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 GGTGCTTTCTGCTACTGCTGCTCTCCATCTTTACTGCA---GAAAGAAAGATCCC 243
Oy 40 AlaPheThrAlaLeuLeuThrThrGlnThrGlnValaGlnArgGlnuLeuValaAsnLysHis 59
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Db 244 GCTTTACTGCTTTGTTAACCCAGCCAGTGCAGAGTCCAAAGGAGATTGTAATTAACAC 303
Oy 60 AsnGlnuLeuArgAlaValaSerProProAlaArgAsnMetLeuLysMetGlnuTrpAsn 79
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Db 304 AATGAAGTAAAGAAAGCAATCTCTCCAGTCCAGTAACATGCTAAAGATGAATGAGAC 363
Oy 80 LysGlnuAlaAlaAlaAsnAlaGlnuLysTrpAlaAsnGlnuLysAsnTyraArgHisSerAsn 99
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Oy 100 ProLysAspArgMetThrSerLeuLysCysGlnuAsnLeuTyMetSerSerAlaPro 119
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Oy 120 SerSerTrpSerGlnAlaIleGlnSerTrpPheAspGlnuTyraAsnAspPheAspPheGly 139
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Oy 140 ValGlyProLysThrProAsnAlaValaIal-GlyHisTyTrhGlnuValaIalTrpTyrse 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 544 GTAGGACCAAGAGTCCCATGCTGTTGGACATTTATACACACTCTTTGGTACTC 603
Oy 159 rSerTrpLeuValaIaGlyAsnAlaTyrcysProAsnGlnuLysValaLeuLysTyTy 179
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Oy 179 rTyValaLysGlnuTyrcysProAlaGlnuAsnTyraAsnArgLeuTyValaProTyrG 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 CTATGTTGGCATATTTGCTGCTGCTGTAATATATGAAGAAGAAATCCCGGACCA 723
Oy 199 uGlnGlnuAlaProCysAlaSerCysProAsnAsnCysAspAspGlyLeuLysThrAsnG 219
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Oy 219 yCysLysTyrglnuAspLeu 225
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RESULT 6
BF897404
LOCUS
DEFINITION
BF897404
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 450)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the RPRESF/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=1l2t2-1l2-MT0181-
281100-265-E05t3-2000-11-28t4-1)
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High quality sequence stop: 449.
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1. 450
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from ORESTES PCR (U.S. Letters Patent application No. 196
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into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      138 a      94 c      96 g      122 t
ORIGIN

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Pred. No.:      5.55e-88      Length:      450
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Best Local Similarity: 99.33%      Mismatches: 0
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DB:             12      Gaps:      0

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Db 2 CAAGAAGTGGCAACCAAGTGCATTTACAGACAGTAAACCAAGATGCAATGACAGT 61
Oy 107 LeuLysCysGlnuLysnLeuTyMetSerSerAlaProSerSerTrpSerGlnuAlaIle 126
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 QY 98 RASNPProLysAspArgMetThrSerLeuLysCysGlyLysAsnLeuTYrMetSerSerAl 118
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 QY 118 AProSerSerTrpSerGlnAlaAlaGlnSerTrpPheAspGluTYrAsnAspPheAsp 138
 DB 482 CCTACTCTCTGTCTCTGTCTGCAATCCAAAGCTGATGACGAGATCCTAGATTGTGTGA 541
 QY 138 eGlyValGlyProLysThrProAsnAlaValAlaGlyHisTrpTrpGlnValValTrpTY 158
 DB 542 TGGTGTAGACCAAGAGTCCCAATGCAAGTGTGTGACATTAATCTGAGCTTTGGTA 601
 QY 158 rSerSerTrpLeuValGlyCysGlyAsnAlaAlaTYrCysProAsnGlnLysValLeuLysTY 178
 DB 602 CTCGACTTACCAAGTACAGCTGTGCAATGTCCACTGTCCCAATCAAGATAGCTAAATA 661
 QY 178 rTYrTYrValCysGlnTYrCysProAlaGlyAsnTrpAlaAsnArgLeuTYrValProTY 198
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 QY 198 rGluGlnGlyAlaProCysAlaSerCysProAsnAsnCysAspAspGlyLeuCysThr 217
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 ACCESSION BF897410.1 GI:12288856
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/ICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?el=IL2&ct=IL2-MT0181-
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 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent Application No. 136
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 144 a 96 c 98 g 123 t 3 others
 ORIGIN
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 Best Local Similarity: 96.13% Mismatches: 4
 Query Match: 59.19% Indels: 1
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 DB 62 CGAATGACAGAGCTAAATGTGTGTGAGAACTCTACATGTCAAGGCCGCCAGCTCATAG 121
 QY 123 SerGlnAlaAlaGlnSerTrpPheAspGluTYrAsnAspPheAspPheGlyValAlaPro 142
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 QY 163 ValGlyCysGlyAsnAlaAlaTYrCysProAsnGlnLysValLeuLysTYrTYrValCys 182
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 QY 183 GlnTYrCysProAlaGlyAsnTrpAlaAsnArgLeuTYrValProTYrGluGlnGlyAla 202
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 DB 362 CCTGTGCGAGTGTCCCAATACGTGTGACGATGGACTATGGCACCAAATGTTGCCAAGTAC 421
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 ACCESSION BF897412
 VERSION BF897412.1 GI:12288858
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 451)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. The Jackson Laboratory

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DB 262 AAGGTTCTAAATACTACTATGTTTCCCAATATGTTCTGCTGTAATGGCTAATAG 203
QY 194 LeuTyrValProTyrGlnGlnGlyAlaProCysAlaSerCysProAspAsnCysAsp 213
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QY 214 GlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsnGlySerLeuLys 233
DB 142 GACCTATGACCAATGCTGCAAGTACGAGATCTCTATAGTAACTGTAAGTTTGAAG 83
QY 234 LeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLysAlaSerCysAsnGly 253
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QY 254 SerAsnSerTyrTyr 258
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DEFINITION 603075145F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167186 5',
ACCESSION BI830749
VERSION BI830749.1 GI:15942299
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@b-riemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1415 row: 1 column: 11
High quality sequence stop: 827.
Location/Qualifiers
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directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT 278 a 201 c 193 g 232 t
ORIGIN

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Score: 823.50 Matches: 170
Percent Similarity: 75.95% Conservative: 29
Best Local Similarity: 64.89% Mismatches: 50
Query Match: 57.35% Indels: 14
DB: 13 Gaps: 5
US-09-698-781-3 (1-258) x BI830749 (1-904)
QY 1 MetLysGlnIleLeuHisProAlaLeuGluThr-Thr-----AlaMetThrLeuPhePr 18
DB 125 ATAAATAGATATTTATCTCTGCTGAGAAACCAATTTCCGCAATGCTTACTAC 184
QY 18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
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QY 58 sHisAsnGluLeuValArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
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QY 78 pAsnLysGluAlaAlaAlaAsnAlaGlnLysTyrPalaAsnGlnCysAsnTyrArgHisSe 98
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DB 479 CCTACTTCTGCTGCTGCTGCAATCAAGCTGTATGACAGATCTTATTTGTC-TA 537
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DB 538 TGGTGTAGAGACCAAGAACGCCAATGACAGTGTGAGCACTTATACACACTGTTGTGTA 597
QY 158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyr 178
DB 598 CTGCACTTACCAAGTAGGCTGTGCAATGCTTACTCTCCAAACAGATAGTAAATAA 657
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QY 198 yGlnGlnGlyAlaProCys-AlaSerCysProAspAsnCysAspAspGly---LeuCys 216
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LOCUS IL2-MT0181-281100-265-A06 MT0181 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF897378
ACCESSION BF897378
VERSION BF897378.1 GI:12288837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 420)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

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Alignment Scores:

1.47e-82 Length:

904

